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(54) Title: EPITHELIAL PROTEIN LOST IN NEOPLASM (EPLIN)

(57) Abstract: Polynucleotide and polypeptide sequences encoding a novel tumor suppressor protein, EPLIN, are provided. Also included is a method for detecting a cell proliferative disorder associated with EPLIN. EPLIN is a marker that can be used diagnostically, prognostically and therapeutically over the course of cell proliferative disorders associated with EPLIN.

EPITHELIAL PROTEIN LOST IN NEOPLASM (EPLIN)

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority from U.S. Provisional Application Serial No. 60/153,024, filed September 8, 1999, the disclosure of which is incorporated herein by reference.

FIELD OF THE INVENTION

This invention relates generally to gene expression in normal and neoplastic cells, and specifically to a novel tumor suppressor gene, EPLIN (epithelial protein lost in neoplasm), and its gene products.

BACKGROUND OF THE INVENTION

Progression of cancer in humans is associated with accumulation of genetic mutations. Most genes mutated in cancer are involved primarily in the maintenance of genomic integrity (Lengauer *et al.*, *Nature*, 396:643, 1998) and the control of cell cycle progression (Sherr, *Genes and Devel.*, 12:2984, 1998). These mutations in turn affect expression of a larger number of cellular genes which collectively are responsible for the changes in cell phenotype. Some of the differentially expressed genes function as oncogenes, while others behave as tumor suppressors to facilitate the development or progression of cancer (Weinberg, *Annals of the New York Acad. of Sci.*, 758:331, 1995). As the number of genes that are differentially expressed in cancer far exceed the number of mutated genes, they provide an abundant source of targets that can be exploited to dissect the complex changes that underlie cellular transformation.

Cancer genes are broadly classified into "oncogenes" which, when activated, promote tumorigenesis, and "tumor suppressor genes" which, when nonfunctional, fail to suppress tumorigenesis. While these classifications provide a useful method for conceptualizing tumorigenesis, it is also possible that a particular gene may play differing roles depending upon the particular allelic form of that gene, its regulatory elements, the genetic background and the tissue environment in which it is operating.

Oncogenes are somatic cell genes that are mutated from their wild-type alleles (the art refers to these wild-type alleles as protooncogenes) into forms which are able to induce tumorigenesis under certain conditions. There is presently a substantial literature on known and putative oncogenes and the various alleles of these oncogenes.

Tumor suppressor genes are genes that, in their wild-type alleles, express proteins that suppress abnormal cellular proliferation. When the gene coding for a tumor suppressor protein is mutated, deleted or transcriptionally nonfunctional, the resulting absence of wild-type tumor suppressor protein expression promotes abnormal cellular proliferation. A number of well-studied human tumors and tumor cell lines have been shown to have missing or nonfunctional tumor suppressor genes. Examples of tumor suppression genes include, but are not limited to, the retinoblastoma susceptibility gene or RB gene, the p53 gene, the deleted in colon carcinoma (DCC) gene and the neurofibromatosis type 1 (NF-1) tumor suppressor gene (Weinberg, R. A. *Science*, 1991, 254:1138). Loss of function or inactivation of tumor suppressor genes may play a central role in the initiation and/or progression of a significant number of human cancers.

The present invention shows that many cancers exhibit decreased EPLIN expression relative to their tissues of origin. The limitation and failings of the prior art to provide meaningful markers which correlate with the presence of cell proliferative disorders, such as cancer, has created a need for markers which can be used diagnostically, prognostically, and therapeutically over the course of such disorders. The present invention fulfills such a need.

SUMMARY OF THE INVENTION

The present invention is based on the seminal discovery of a novel tumor suppressor gene, EPLIN (epithelial protein lost in neoplasm), the expression of which is altered in multiple common human tumor types. The invention provides EPLIN polypeptides (SEQ ID NO:2 and SEQ ID NO:4) as well as polynucleotide sequences encoding the polypeptides (SEQ ID NO:1 and SEQ ID NO:3) and antibodies which bind to the polypeptides set forth in SEQ ID NO:2 and SEQ ID NO:4. Thus, it is an object of the present invention to provide a substantially purified EPLIN polypeptide and nucleic acid encoding the EPLIN polypeptide. In accordance with another aspect of the invention, an expression vector containing EPLIN

nucleic acid is provided. Also included is a method for producing the EPLIN polypeptides and antibodies which bind to the EPLIN polypeptides.

In yet another aspect, the invention provides a method for identifying a compound which binds to EPLIN polypeptide that includes incubating components comprising the compound and EPLIN polypeptide under conditions sufficient to allow the components to interact and measuring the binding of the compound to EPLIN polypeptide.

In another aspect, the present invention provides a method of detecting a neoplastic cell in a sample by contacting a sample suspected of containing a neoplastic cell with a reagent that binds to an EPLIN-specific cell component and detecting binding of the reagent to the component.

In another aspect, the invention provides a method of detecting a cell proliferative disorder in a sample from a subject by contacting a first sample having, or suspected of having, a cell proliferative disorder with a reagent that binds to an EPLIN-specific cell component and detecting binding of the reagent to the component; contacting a second cell not having a cell proliferative disorder with a reagent that binds to an EPLIN-specific cell component and detecting binding of the reagent to the component; comparing the level of binding in the first sample with the level of binding in the second sample, wherein a decreased level of binding of the reagent to an EPLIN-specific cell component from the first sample is indicative of a cell proliferative disorder.

A kit useful for the detection of an EPLIN-specific cell component, the kit comprising carrier means containing one or more containers comprising a first container containing an EPLIN-specific binding reagent.

In yet another aspect, the present invention provides a method of ameliorating a cell proliferative disorder associated with EPLIN, comprising administering to a subject with the disorder, a therapeutically effective amount of reagent which regulates EPLIN activity.

In a further aspect, the invention provides a method of gene therapy comprising introducing into cells of a host subject, an expression vector comprising a nucleotide sequence encoding EPLIN, in operable linkage with a promoter.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating preferred embodiments of the

invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A shows a schematic diagram of two EPLIN cDNAs. The sequence of two isoforms diverge at the 5' end (indicated by the stripped and dotted boxes).

Figure 1B shows the deduced amino acid sequence of EPLIN-β.

Figure 1C shows the alignment of the EPLIN LIM domain sequence with the LIM domain of the mutant SREBP-2, KIAA0750, plant transcription factor SF3, and muscle LIM protein.

Figure 2A shows that EPLIN is preferentially expressed in epithelial cells as determined by Northern analysis.

Figure 2B shows the expression of EPLIN in different human primary cells by an immunoblot analysis.

Figure 3A shows, by Northern analysis, that the expression of EPLIN transcript is lost in epithelial cancer cells.

Figure 3B shows the expression of EPLIN proteins in different prostate cancer cell lines and xenograft tumors as determined by an immunoblot analysis.

Figure 3C shows the expression of EPLIN proteins in different breast cancer cell lines as determined by an immunoblot analysis.

Figure 3D shows the expression of EPLIN transcripts in different breast cancer cell lines as determined by a Northern analysis.

Figure 4A shows the relative amount of EPLIN isoforms in HOK18C (a HPV-immortalized human oral keratinocyte cell line) and BeWo (a human choriocarcinoma cell line) as determined by an immunoblot analysis.

Figure 4B shows the subcellular localization of EPLIN as determined by *in situ* immunofluorescence using anti-EPLIN antibodies and Texas Red-conjugated goat anti-rabbit IgG secondary antibody.

Figure 4C shows the staining of actin stress fibers with Oregon Green-phalloidin.

Figure 4D shows the subcellular localization of EPLIN as determined by *in situ* immunofluorescence using anti-EPLIN antibodies and fluorescein isothiocyanate-conjugated goat anti-rabbit IgG secondary antibody.

Figure 4E shows the staining of actin stress fibers with Texas Red-phalloidin.

Figure 5A shows U2-OS osteosarcoma cultured without expression of EPLIN-α.

Figure 5B shows U2-OS osteosarcoma cultured with expression of EPLIN-α.

Figure 5C shows U2-OS osteosarcoma cultured without expression of EPLIN-β.

Figure 5D shows U2-OS osteosarcoma cultured with expression of EPLIN-β.

Figure 5E shows the levels of EPLIN expression in the U2-OS cells cultures minus (no induction) and plus (induction) doxycycline as determined by an immunoblot analysis.

Figure 5F shows the growth of U2-OS cells presented as the ratio of cell numbers with and without EPLIN induction.

DETAILED DESCRIPTION

Various genes are differentially expressed in human cancers. The present invention provides the novel tumor suppressor gene EPLIN (epithelial protein lost in neoplasm) encoding novel cytoskeletal proteins preferentially expressed in human epithelial cells. Two EPLIN isoforms, a 600 amino acid EPLIN-α (SEQ ID NO:2) and a 759 amino acid EPLIN-β (SEQ ID NO:4), are detected in primary epithelial cells of oral mucosa, prostate and mammary glands. Both EPLIN isoforms localize to filamentous actin and suppress cell proliferation when overexpressed. Thus, the invention further provides a polynucleotide (SEQ ID NO:1) encoding the amino acid sequence for EPLIN-α and a polynucleotide (SEQ ID NO:3) encoding the amino acid sequence for EPLIN-β. These findings indicate that the loss of EPLIN seen in cancer cells may play a role in cancer progression. Based on this discovery, it is an object of the invention to provide compounds, and pharmaceutical compositions thereof, which modulate cell proliferation.

The EPLIN protein, fragments thereof, and derivatives and other variants of the sequence in SEQ ID NO:2 or SEQ ID NO:4 thereof are collectively referred to as "polypeptides or proteins of the invention" or "EPLIN polypeptides or proteins." Nucleic acid molecules encoding such polypeptides or proteins are collectively referred to as "nucleic

acids of the invention" or "EPLIN nucleic acids." EPLIN molecules refer to EPLIN nucleic acids, polypeptides, and antibodies.

As used herein, the term "nucleic acid molecule" includes DNA molecules (*e.g.*, a cDNA or genomic DNA) and RNA molecules (*e.g.*, an mRNA) and analogs of the DNA or RNA generated, *e.g.*, by the use of nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

The term "isolated or purified nucleic acid molecule" includes nucleic acid molecules that are separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. For example, with respect to genomic DNA, the term "isolated" includes nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. Preferably, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and/or 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of 5' and/or 3' nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

As used herein, the term "hybridizes under stringent conditions" describes conditions for hybridization and washing. Stringent conditions are known to those skilled in the art and can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Aqueous and nonaqueous methods are described in that reference and either can be used. A preferred example of stringent hybridization conditions includes hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50°C. Another example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 55°C. A further example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 60°C. Preferably, stringent

hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C. Particularly preferred stringency conditions (and the conditions that should be used if the practitioner is uncertain about what conditions should be applied to determine if a sequence is within the invention) are 0.5M Sodium Phosphate, 7% SDS at 65°C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NOs:1 or 3, corresponds to a naturally occurring nucleic acid molecule.

As used herein, a "naturally occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules that include an open reading frame encoding an EPLIN protein, preferably a mammalian EPLIN protein, and further can include non-coding regulatory sequences and introns.

An "isolated" or "purified" polypeptide or protein is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. In one embodiment, the language "substantially free" means preparation of EPLIN protein having less than about 30%, 20%, 10% and more preferably 5% (by dry weight), of non-EPLIN protein (also referred to herein as a "contaminating protein"), or of chemical precursors or non-EPLIN chemicals. When the EPLIN protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The invention includes isolated or purified preparations of at least 0.01, 0.1, 1.0, and 10 milligrams in dry weight.

A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of EPLIN (*e.g.*, the sequence of SEQ ID NO:2 or 4) without abolishing or more preferably, without substantially altering a biological activity of the EPLIN protein, whereas an "essential" amino acid residue results in such a change. For example, amino acid

residues that are conserved among the polypeptides of the present invention are predicted to be particularly unamenable to alteration.

A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an EPLIN protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an EPLIN coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for EPLIN biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:1 or 3, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

As used herein, a "biologically active portion" of an EPLIN protein includes a fragment of an EPLIN protein that participates in an interaction between an EPLIN molecule and a non-EPLIN molecule. Biologically active portions of an EPLIN protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the EPLIN protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2, which include less amino acids than the full length EPLIN protein and exhibit at least one activity of an EPLIN protein, such as tumor suppressor activity. Typically, biologically active portions comprise a domain or motif with at least one activity of the EPLIN protein. A biologically active portion of an EPLIN protein can be a polypeptide that is, for example, 10, 25, 50, 100, 200, 300 or more amino acids in length. Biologically active portions of an EPLIN protein can be used as targets for developing agents that modulate an EPLIN mediated activity.

Calculations of homology or sequence identity between sequences (the terms are used interchangeably herein) are performed as follows. To determine the percent identity of two

amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, 90%, 100% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch ((1970) *J. Mol. Biol.*, 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within the invention) is using a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

The percent identity between two amino acid or nucleotide sequences can be determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989))

which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.*, 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to EPLIN nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to EPLIN protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.*, 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov.

"Misexpression or aberrant expression," as used herein, refers to a non-wild type pattern of gene expression at the RNA or protein level. It includes: expression at non-wild type levels, *i.e.*, over or underexpression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, *e.g.*, increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-transitional modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, *e.g.*, a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

"Subject," as used herein, can refer to a mammal, *e.g.*, a human, or to an experimental animal or disease model. The subject also can be a non-human animal, *e.g.*, a horse, cow, goat, or other domestic animal.

Thus, in a first embodiment, the present invention provides substantially pure EPLIN polypeptides consisting essentially of the amino acid sequence of SEQ ID NO:2 and SEQ ID NO:4. The term "substantially pure" as used herein refers to EPLIN polypeptide that is substantially free of other proteins, lipids, carbohydrates or other materials with which it is naturally associated. One skilled in the art can purify EPLIN using standard techniques for protein purification. The substantially pure polypeptide will yield a single major band on a non-reducing polyacrylamide gel. The purity of an EPLIN polypeptide can also be determined by amino-terminal amino acid sequence analysis.

The invention includes functional polypeptides of EPLIN-α and EPLIN-β, and functional fragments thereof. As used herein, the term "functional polypeptide" refers to a polypeptide which possesses a biological function or activity which is identified through a defined functional assay and which is associated with a particular biologic, morphologic, or phenotypic alteration in the cell. Functional fragments of the EPLIN polypeptide, includes fragments of EPLIN as long as the activity, *e.g.*, tumor suppressor activity, of EPLIN remains. Smaller peptides containing the biological activity of EPLIN are included in the invention. The biological function, for example, can vary from a polypeptide fragment as small as an epitope to which an antibody molecule can bind to a large polypeptide which is capable of participating in the characteristic induction or programming of phenotypic changes within a cell. A "functional polynucleotide" denotes a polynucleotide that encodes a functional polypeptide as described herein.

As previously noted, minor modifications of the EPLIN primary amino acid sequence may result in proteins that have substantially equivalent activity as compared to the EPLIN polypeptide described herein. Such modifications may be deliberate, as by site-directed mutagenesis, or may be spontaneous. All of the polypeptides produced by these modifications are included herein as long as the tumor suppressor activity of EPLIN is present. Further, deletion of one or more amino acids can also result in a modification of the structure of the resultant molecule without significantly altering its activity. This can lead to the development of a smaller active molecule that would have broader utility. For example, it is possible to remove amino or carboxy terminal amino acids that may not be required for EPLIN activity.

The invention also provides an isolated polynucleotide sequence consisting essentially of a polynucleotide sequence encoding a polypeptide having the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4. The term "isolated" as used herein includes polynucleotides substantially free of other nucleic acids, proteins, lipids, carbohydrates or other materials with which it is naturally associated. Polynucleotide sequences of the invention include DNA, cDNA and RNA sequences that encode EPLIN. It is understood that all polynucleotides encoding all or a portion of EPLIN are also included herein, as long as they encode a polypeptide with EPLIN activity. Such polynucleotides include naturally occurring, synthetic, and intentionally manipulated polynucleotides. For example, EPLIN polynucleotide may be subjected to site-directed mutagenesis. The polynucleotide sequence for EPLIN also includes antisense sequences. The polynucleotides of the invention include sequences that are degenerate as a result of the genetic code. There are 20 natural amino acids, most of which are specified by more than one codon. Therefore, all degenerate nucleotide sequences are included in the invention as long as the amino acid sequence of EPLIN polypeptide encoded by the nucleotide sequence is functionally unchanged. In addition, the invention also includes a polynucleotide consisting essentially of a polynucleotide sequence encoding a polypeptide having an amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 and having at least one epitope for an antibody immunoreactive with EPLIN polypeptide.

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence shown in SEQ ID NO:1 or 3. Such differences can be due to degeneracy of the genetic code (and result in a nucleic acid that encodes the same EPLIN proteins as those encoded by the nucleotide sequence disclosed herein. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence that differs by at least 1, but less than 5, 10, 20, 50, or 100 amino acid residues than that shown in SEQ ID NO:2 or 4. If alignment is needed for this comparison the sequences should be aligned for maximum homology. "Looped" out sequences from deletions, insertions, or mismatches, are considered differences.

Nucleic acids of the invention can be chosen for having codons, which are preferred or non-preferred, for a particular expression system. *E.g.*, the nucleic acid can be one in which at least one codon, at preferably at least 10%, or 20% of the codons has been altered

such that the sequence is optimized for expression in *E. coli*, yeast, human, insect, or chinese hamster ovary (CHO) cells.

Nucleic acid variants can be naturally occurring, such as allelic variants (same locus), homologs (different locus), and orthologs (different organism) or can be non-naturally occurring. Non-naturally occurring variants can be made by mutagenesis techniques, including those applied to polynucleotides, cells, or organisms. The variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared with the encoded product).

In a preferred embodiment, the nucleic acid differs from that of SEQ ID NO:1 or 3 as follows: by at least one but less than 10, 20, 30, or 40 nucleotides; at least one but less than 1%, 5%, 10% or 20% of the nucleotides in the subject nucleic acid. If necessary for this analysis, the sequences should be aligned for maximum homology. "Looped" out sequences from deletions, insertions, or mismatches, are considered differences.

Orthologs, homologs, and allelic variants can be identified using methods known in the art. These variants comprise a nucleotide sequence encoding a polypeptide that is 50%, at least about 55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically at least about 90-95% or more identical to the amino acid sequence shown in SEQ ID NO:2 or a fragment of this sequence. Such nucleic acid molecules can readily be identified as being able to hybridize under stringent conditions, to the nucleotide sequence shown in SEQ ID NO 1 or a fragment of the sequence. Nucleic acid molecules corresponding to orthologs, homologs, and allelic variants of the EPLIN cDNAs of the invention can further be isolated by mapping to the same chromosome or locus as the EPLIN gene. Preferred variants include those that are correlated with a tumor suppressor activity.

Allelic variants of EPLIN, *e.g.*, human EPLIN, include both functional and non-functional proteins. Functional allelic variants are naturally occurring amino acid sequence variants of the EPLIN protein within a population that maintain the ability to function as a tumor suppressor protein. Functional allelic variants typically will contain only conservative substitution of one or more amino acids of SEQ ID NO:2 or 4, or substitution, deletion or insertion of non-critical residues in non-critical regions of the protein. Non-functional allelic variants are naturally occurring amino acid sequence variants of the EPLIN, *e.g.*, human

EPLIN. Non-functional allelic variants will typically contain a non-conservative substitution, a deletion, or insertion, or premature truncation of the amino acid sequence of SEQ ID NO:2, or a substitution, insertion, or deletion in critical residues or critical regions of the protein.

Polynucleotides encoding EPLIN include the nucleotide sequence of SEQ ID NO:1 and SEQ ID NO:3, as well as nucleic acid sequences complementary to those sequences sequence. A complementary sequence may include an antisense nucleotide. When the sequence is RNA, the deoxynucleotides A, G, C, and T of SEQ ID NO:1 are replaced by ribonucleotides A, G, C, and U, respectively. Also included in the invention are fragments of the above-described nucleic acid sequences that are at least 15 bases in length, which is sufficient to permit the fragment to selectively hybridize to DNA that encodes the polypeptide of SEQ ID NO:2 or SEQ ID NO:4 under physiological conditions.

In another aspect, the invention features, an isolated nucleic acid molecule that is antisense to EPLIN. An "antisense" nucleic acid can include a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. The antisense nucleic acid can be complementary to an entire EPLIN coding strand, or to only a portion thereof (*e.g.*, the coding region of EPLIN corresponding to SEQ ID NO:3). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding EPLIN (*e.g.*, the 5' and 3' untranslated regions).

An antisense nucleic acid can be designed such that it is complementary to the entire coding region of EPLIN mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of EPLIN mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of EPLIN mRNA, *e.g.*, between the -10 and +10 regions of the target gene nucleotide sequence. An antisense oligonucleotide can be, for example, about 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or more nucleotides in length.

An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions with procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized

using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. The antisense nucleic acid also can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject (*e.g.*, by direct injection at a tissue site), or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an EPLIN protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong polymerase II or polymerase III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.*, 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.*, 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.*, 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. A ribozyme having specificity for an EPLIN-encoding nucleic acid can include one or more sequences complementary to the nucleotide sequence of an EPLIN cDNA disclosed herein

(*i.e.*, SEQ ID NO:1 or 3), and a sequence having known catalytic sequence responsible for mRNA cleavage (see U.S. Pat. No. 5,093,246 or Haselhoff and Gerlach (1988) *Nature*, 334:585-591). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an EPLIN-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, EPLIN mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science*, 261:1411-1418.

EPLIN gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the EPLIN (*e.g.*, the EPLIN promoter and/or enhancers) to form triple helical structures that prevent transcription of the EPLIN gene in target cells. See, generally, Helene, C. (1991) *Anticancer Drug Des.*, 6(6):569-84; Helene, C. *et al.* (1992) Ann. N.Y. Acad. Sci., 660:27-36; and Maher, L.J. (1992) *Bioassays*, 14(12):807-15. The potential sequences that can be targeted for triple helix formation can be increased by creating a "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

DNA sequences of the invention can be obtained by several methods. For example, the DNA can be isolated using hybridization techniques that are well known in the art. These include, but are not limited to: (1) hybridization of genomic or cDNA libraries with probes to detect homologous nucleotide sequences and (2) antibody screening of expression libraries to detect cloned DNA fragments with shared structural features.

Preferably the EPLIN polynucleotide of the invention is derived from a mammalian organism, and most preferably from human. Screening procedures that rely on nucleic acid hybridization make it possible to isolate any gene sequence from any organism, provided the appropriate probe is available. Oligonucleotide probes, which correspond to a part of the sequence encoding the protein in question, can be synthesized chemically. This requires that short, oligopeptide stretches of amino acid sequence must be known. The DNA sequence encoding the protein can be deduced from the genetic code, however, the degeneracy of the

code must be taken into account. It is possible to perform a mixed addition reaction when the sequence is degenerate. This includes a heterogeneous mixture of denatured double-stranded DNA. For such screening, hybridization is preferably performed on either single-stranded DNA or denatured double-stranded DNA. Hybridization is particularly useful in the detection of cDNA clones derived from sources where an extremely low amount of mRNA sequences relating to the polypeptide of interest are present. In other words, by using stringent hybridization conditions directed to avoid non-specific binding, it is possible, for example, to allow the autoradiographic visualization of a specific cDNA clone by the hybridization of the target DNA to that single probe in the mixture that is its complete complement (Wallace *et al.*, *Nucl. Acid Res.*, 9:879, 1981).

The development of specific DNA sequences encoding EPLIN can also be obtained by: (1) isolation of double-stranded DNA sequences from the genomic DNA; (2) chemical manufacture of a DNA sequence to provide the necessary codons for the polypeptide of interest; and (3) *in vitro* synthesis of a double-stranded DNA sequence by reverse transcription of mRNA isolated from a eukaryotic donor cell. In the latter case, a double-stranded DNA complement of mRNA is eventually formed which is generally referred to as cDNA.

Of the three above-noted methods for developing specific DNA sequences for use in recombinant procedures, the isolation of genomic DNA isolates is the least common. This is especially true when it is desirable to obtain the microbial expression of mammalian polypeptides due to the presence of introns.

The synthesis of DNA sequences is frequently the method of choice when the entire sequence of amino acid residues of the desired polypeptide product is known. When the entire sequence of amino acid residues of the desired polypeptide is not known, the direct synthesis of DNA sequences is not possible and the method of choice is the synthesis of cDNA sequences. Among the standard procedures for isolating cDNA sequences of interest is the formation of plasmid- or phage-carrying cDNA libraries that are derived from reverse transcription of mRNA which is abundant in donor cells that have a high level of genetic expression. When used in combination with polymerase chain reaction technology, even rare expression products can be cloned. In those cases where significant portions of the amino acid sequence of the polypeptide are known, the production of labeled single or double-

stranded DNA or RNA probe sequences duplicating a sequence putatively present in the target cDNA may be employed in DNA/DNA hybridization procedures which are carried out on cloned copies of the cDNA which have been denatured into a single-stranded form (Jay *et al.*, *Nucl. Acid Res.*, 11:2325, 1983).

A cDNA expression library, such as lambda gt11, can be screened indirectly for EPLIN peptides having at least one epitope, using antibodies specific for EPLIN. Such antibodies can be either polyclonally or monoclonally derived and used to detect expression product indicative of the presence of EPLIN cDNA.

DNA sequences encoding EPLIN can be expressed *in vitro* by DNA transfer into a suitable host cell. "Host cells" are cells in which a vector can be propagated and its DNA expressed. The term also includes any progeny of the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. However, such progeny are included when the term "host cell" is used. Methods of stable transfer, meaning that the foreign DNA is continuously maintained in the host, are known in the art.

In the present invention, the EPLIN polynucleotide sequences may be inserted into a recombinant expression vector. The term "recombinant expression vector" refers to a plasmid, virus or other vehicle known in the art that has been manipulated by insertion or incorporation of the EPLIN genetic sequences. Such expression vectors contain a promoter sequence which facilitates the efficient transcription of the inserted genetic sequence of the host. The expression vector typically contains an origin of replication, a promoter, as well as specific genes which allow phenotypic selection of the transformed cells. Vectors suitable for use in the present invention include, but are not limited to the T7-based expression vector for expression in bacteria (Rosenberg *et al.*, *Gene*, 56:125, 1987), the pMSXND expression vector for expression in mammalian cells (Lee and Nathans, *J. Biol. Chem.*, 263:3521, 1988) and baculovirus-derived vectors for expression in insect cells. The DNA segment can be present in the vector operably linked to regulatory elements, for example, a promoter (*e.g.*, T7, metallothionein I, or polyhedrin promoters).

Polynucleotide sequences encoding EPLIN can be expressed in either prokaryotes or eukaryotes. Hosts can include microbial, yeast, insect, and mammalian organisms. Methods of expressing DNA sequences having eukaryotic or viral sequences in prokaryotes are well

known in the art. Biologically functional viral and plasmid DNA vectors capable of expression and replication in a host are known in the art. Such vectors are used to incorporate DNA sequences of the invention.

In another aspect, the invention provides EPLIN chimeric or fusion proteins. As used herein, an EPLIN "chimeric protein" or "fusion protein" includes an EPLIN polypeptide linked to a non-EPLIN polypeptide. A "non-EPLIN polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the EPLIN protein, *e.g.*, a protein that is different from the EPLIN protein and that is derived from the same or a different organism. The EPLIN polypeptide of the fusion protein can correspond to all or a portion *e.g.*, a fragment described herein of an EPLIN amino acid sequence. In a preferred embodiment, an EPLIN fusion protein includes at least one (*e.g.* two) biologically active portion of an EPLIN protein. The non-EPLIN polypeptide can be fused to the N-terminus or C-terminus of an EPLIN polypeptide.

The fusion protein can include a moiety that has high affinity for a ligand. For example, the fusion protein can be a GST-EPLIN fusion protein in which the EPLIN sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant EPLIN. Alternatively, the fusion protein can be an EPLIN protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of EPLIN can be increased through use of a heterologous signal sequence.

Fusion proteins can include all or a part of a serum protein, *e.g.*, an IgG constant region, or human serum albumin.

The EPLIN fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject in vivo. The EPLIN fusion proteins can be used to affect the bioavailability of an EPLIN substrate. EPLIN fusion proteins may be useful therapeutically for the treatment of disorders caused by, for example: (i) aberrant modification or mutation of a gene encoding an EPLIN protein; (ii) mis-regulation of the EPLIN gene; and (iii) aberrant post-translational modification of an EPLIN protein.

Moreover, EPLIN-fusion proteins of the invention can be used as immunogens to produce anti-EPLIN antibodies in a subject, to purify EPLIN ligands, and in screening assays to identify molecules that inhibit the interaction of EPLIN with an EPLIN substrate.

Expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An EPLIN-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the EPLIN protein.

In another aspect, the invention features a variant of an EPLIN polypeptide, *e.g.*, a polypeptide that functions as an agonist (mimetic) or as an antagonist of EPLIN activities. Variants of the EPLIN proteins can be generated by mutagenesis, *e.g.*, discrete point mutations, the insertion or deletion of sequences or the truncation of an EPLIN protein. An agonist of the EPLIN protein retains substantially the same, or a subset, of the biological activities of the naturally occurring form of an EPLIN protein. An antagonist of an EPLIN protein can inhibit one or more of the activities of the naturally occurring form of the EPLIN protein by, for example, competitively modulating an EPLIN-mediated activity of an EPLIN protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Preferably, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the EPLIN protein.

Variants of an EPLIN protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of an EPLIN protein for agonist or antagonist activity.

Libraries of fragments *e.g.*, N terminal, C terminal, or internal fragments, of an EPLIN protein coding sequence can be used to generate a variegated population of fragments for screening and subsequent selection of variants of an EPLIN protein.

Variants in which a cysteine residue is added or deleted or in which a residue that is glycosylated is added or deleted are particularly preferred.

Methods for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property are known. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with screening assays to identify EPLIN variants (Arkin and Yourvan (1992) *Proc. Natl. Acad. Sci. USA*, 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering*, 6(3):327-331).

Cell based assays can be exploited to analyze a variegated EPLIN library. For example, a library of expression vectors can be transfected into a cell line, *e.g.*, a cell line,

which ordinarily responds to EPLIN in a substrate-dependent manner. The transfected cells are then contacted with EPLIN and the effect of the expression of the mutant on signaling by the EPLIN substrate can be detected, *e.g.*, by measuring tumor suppressor activity in an appropriate assay. Plasmid DNA can then be recovered from the cells that score for inhibition, or alternatively, potentiation of signaling by the EPLIN substrate, and the individual clones further characterized.

In another aspect, the invention features a method of making an EPLIN polypeptide, *e.g.*, a peptide having a non-wild type activity, *e.g.*, an antagonist, agonist, or super agonist of a naturally occurring EPLIN polypeptide, *e.g.*, a naturally occurring EPLIN polypeptide. The method includes: altering the sequence of an EPLIN polypeptide, *e.g.*, by substitution or deletion of one or more residues of a non-conserved region, a domain, or residue disclosed herein, and testing the altered polypeptide for the desired activity.

In another aspect, the invention features a method of making a fragment or analog of an EPLIN polypeptide that retains at least one biological activity of a naturally occurring EPLIN polypeptide. The method includes: altering the sequence, *e.g.*, by substitution or deletion of one or more residues, of an EPLIN polypeptide, *e.g.*, altering the sequence of a non-conserved region, or a domain or residue described herein, and testing the altered polypeptide for the desired activity.

Screening Method

EPLIN nucleic acids, proteins, and derivatives of the present invention also have uses in screening assays to detect molecules that specifically bind to EPLIN nucleic acids, proteins, or derivatives and thus have potential use as agonists or antagonists of EPLIN, in particular, molecules that affect cell proliferation. In one embodiment, such assays are performed to screen for molecules with potential utility as anti-cancer drugs or lead compounds for drug development. The invention provides assays to detect molecules that specifically bind to EPLIN nucleic acids, proteins, or derivatives. For example, recombinant cells expressing EPLIN nucleic acids can be used to recombinantly produce EPLIN proteins in these assays, to screen for molecules that bind to an EPLIN protein. Molecules (*e.g.*, putative binding partners of EPLIN) are contacted with the EPLIN protein (or fragment thereof) under conditions conducive to binding, and then molecules that specifically bind to

the EPLIN protein are identified. Similar methods can be used to screen for molecules that bind to EPLIN derivatives or nucleic acids. Methods that can be used to carry out the foregoing are commonly known in the art.

By way of example, diversity libraries, such as random or combinatorial peptide or nonpeptide libraries can be screened for molecules that specifically bind to EPLIN. Many libraries are known in the art that can be used, *e.g.*, chemically synthesized libraries, recombinant (*e.g.*, phage display libraries), and *in vitro* translation-based libraries.

For example, agonists and antagonists of EPLIN can be identified using "biochip" technology. "Biochips" or arrays of binding agents, such as oligonucleotides and peptides, have become an increasingly important tool in the biotechnology industry and related fields.

These binding agent arrays, in which a plurality of binding agents are deposited onto a solid support surface in the form of an array or pattern, find use in a variety of applications, including drug screening, nucleic acid sequencing, mutation analysis, and the like. One important use of biochips is in the analysis of differential gene expression, where the expression of genes in different cells, normally a cell of interest and a control, is compared and any discrepancies in expression are identified. In such assays, the presence of discrepancies indicates a difference in the classes of genes expressed in the cells being compared.

In methods of differential gene expression, arrays find use by serving as a substrate to which is bound polynucleotide "probe" fragments. One then obtains "targets" from analogous cells, tissues, or organs of a healthy and diseased organism. The targets are then hybridized to the immobilized set of polynucleotide "probe" fragments. Differences between the resultant hybridization patterns are then detected and related to differences in gene expression in the two sources. Thus, the present invention provides nucleic acid and amino acid sequences useful for screening for differential expression of EPLIN in a cell.

The invention includes antibodies immunoreactive with EPLIN polypeptide or functional fragments thereof. Antibody which consists essentially of pooled monoclonal antibodies with different epitopic specificities, as well as distinct monoclonal antibody preparations are provided. Monoclonal antibodies are made from antigen containing fragments of the protein by methods well known to those skilled in the art (Kohler *et al.*, *Nature*, 256:495, 1975). The term antibody as used in this invention is meant to include

intact molecules as well as fragments thereof, such as Fab and $F(ab')_2$, which are capable of binding an epitopic determinant on EPLIN.

Monoclonal antibodies used in the method of the invention are suited for use, for example, in immunoassays in which they can be utilized in liquid phase or bound to a solid phase carrier. In addition, the monoclonal antibodies in these immunoassays can be detectably labeled in various ways. Examples of types of immunoassays which can utilize monoclonal antibodies of the invention are competitive and non-competitive immunoassays in either a direct or indirect format. Examples of such immunoassays are the radioimmunoassay (RIA) and the sandwich (immunometric) assay. Detection of the antigens using the monoclonal antibodies of the invention can be done utilizing immunoassays which are run in either the forward, reverse, or simultaneous modes, including immunohistochemical assays on physiological samples. Those of skill in the art will know, or can readily discern, other immunoassay formats without undue experimentation.

Diagnostic Uses of EPLIN

EPLIN proteins, analogues, derivatives, and subsequences thereof, EPLIN nucleic acids (and sequences complementary thereto), anti-EPLIN antibodies, have uses in diagnostics. Such molecules can be used in assays, such as immunoassays, to detect, prognose, diagnose, or monitor various conditions, diseases, and disorders affecting EPLIN expression, or monitor the treatment thereof. In particular, such an immunoassay is carried out by a method comprising contacting a sample derived from a patient with an anti-EPLIN antibody under conditions such that immunospecific binding can occur, and detecting or measuring the amount of any immunospecific binding by the antibody. In a specific aspect, such binding of antibody, in tissue sections, can be used to detect aberrant EPLIN localization or aberrant (*e.g.*, low or absent) levels of EPLIN. In a specific embodiment, antibody to EPLIN can be used to assay in a patient tissue or serum sample for the presence of EPLIN where an aberrant level of EPLIN is an indication of a diseased condition. By "aberrant levels," is meant increased or decreased levels relative to that present, or a standard level representing that present, in an analogous sample from a portion of the body or from a subject not having the disorder.

Thus, the invention provides a method of detecting a cell proliferative disorder in a sample from a subject by contacting a first sample having, or suspected of having, a cell proliferative disorder with a reagent that binds to an EPLIN-specific cell component and detecting binding of the reagent to the component; contacting a second cell not having a cell proliferative disorder with a reagent that binds to an EPLIN-specific cell component and detecting binding of the reagent to the component; comparing the level of binding in the first sample with the level of binding in the second sample, wherein a decreased level of binding of the reagent to an EPLIN-specific cell component from the first sample is indicative of a cell proliferative disorder.

The term "cell proliferative disorder," as used herein, refers to a condition characterized by abnormal cell growth. The condition can include both hypertrophic (the continual multiplication of cells resulting in an overgrowth of a cell population within a tissue) and hypotrophic (a lack or deficiency of cells within a tissue) cell growth or an excessive influx or migration of cells into an area of a body. The cell populations are not necessarily transformed, tumorigenic or malignant cells, but also can include normal cells. As used herein, an "EPLIN-specific cell component" includes, but is not limited to, RNA and DNA encoding an EPLIN protein, the EPLIN protein and fragments thereof, and EPLIN variants including translocations in EPLIN nucleic acids, truncations in the EPLIN gene or protein, changes in nucleotide or amino acid sequence relative to wild-type EPLIN.

The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement- fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few.

EPLIN genes and related nucleic acid sequences and subsequences, including complementary sequences, can also be used in hybridization assays. EPLIN nucleic acid sequences, or subsequences thereof comprising about at least 8 nucleotides, can be used as hybridization probes.

Hybridization assays can be used to detect, prognose, diagnose, or monitor conditions, disorders, or disease states associated with aberrant changes in EPLIN expression and/or activity as described. In particular, such a hybridization assay is carried out by a method comprising contacting a sample containing nucleic acid with a nucleic acid probe capable of hybridizing to EPLIN DNA or RNA, under conditions such that hybridization can occur, and detecting or measuring any resulting hybridization.

In specific embodiments, diseases and disorders involving over-proliferation of cells can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting increased levels of EPLIN protein, EPLIN RNA, or EPLIN functional activity or by detecting mutations in EPLIN RNA, DNA or protein (*e.g.*, translocations in EPLIN nucleic acids, truncations in the EPLIN gene or protein, changes in nucleotide or amino acid sequence relative to wild-type EPLIN) that cause increased expression or activity of EPLIN. By way of example, levels of EPLIN protein can be detected by immunoassay, levels of EPLIN RNA can be detected by hybridization assays (*e.g.*, Northern blots, dot blots), translocations and point mutations in EPLIN nucleic acids can be detected by Southern blotting, RFLP analysis, PCR using primers that preferably generate a fragment spanning at least most of the EPLIN gene, sequencing of the EPLIN genomic DNA or cDNA obtained from the patient.

In a preferred embodiment, levels of EPLIN mRNA or protein in a patient sample are detected or measured, in which increased levels indicate that the subject has, or has a predisposition to developing, a malignancy or hyperproliferative disorder; in which the increased levels are relative to the levels present in an analogous sample from a portion of the body or from a subject not having the malignancy or hyperproliferative disorder, as the case may be.

In another specific embodiment, diseases and disorders involving a deficiency in cell proliferation or in which cell proliferation is desirable for treatment, are diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting decreased levels of EPLIN protein, EPLIN RNA, or EPLIN functional activity, or by detecting mutations in EPLIN RNA, DNA or protein (*e.g.*, translocations in EPLIN nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type EPLIN) that cause decreased expression or activity of EPLIN.

By way of example, levels of EPLIN protein, levels of EPLIN RNA, EPLIN binding activity, and the presence of translocations or point mutations can be determined as described.

In a specific embodiment, levels of EPLIN mRNA or protein in a patient sample are detected or measured, in which decreased levels indicate that the subject has, or has a predisposition to developing, a malignancy or hyperproliferative disorder; in which the decreased levels are relative to the levels present in an analogous sample from a portion of the body or from a subject not having the malignancy or hyperproliferative disorder, as the case may be.

In using a monoclonal antibody for the *in vivo* detection of antigen, the detectably labeled monoclonal antibody is given in a dose which is diagnostically effective. The term "diagnostically effective" means that the amount of detectably labeled monoclonal antibody is administered in sufficient quantity to enable detection of the site having the EPLIN antigen for which the monoclonal antibodies are specific. The concentration of detectably labeled monoclonal antibody which is administered should be sufficient such that the binding to those cells having EPLIN is detectable compared to the background. Further, it is desirable that the detectably labeled monoclonal antibody be rapidly cleared from the circulatory system in order to give the best target-to-background signal ratio.

As a rule, the dosage of detectably labeled monoclonal antibody for *in vivo* diagnosis will vary depending on such factors as age, sex, and extent of disease of the individual. The dosage of monoclonal antibody can vary from about 0.001 mg/m^2 to about 500 mg/m^2, preferably 0.1 mg/m^2 to about 200 mg/m^2, most preferably about 0.1 mg/m^2 to about 10 mg/m^2. Such dosages may vary, for example, depending on whether multiple injections are given, tumor burden, and other factors known to those of skill in the art.

For *in vivo* diagnostic imaging, the type of detection instrument available is a major factor in selecting a given radioisotope. The radioisotope chosen must have a type of decay which is detectable for a given type of instrument. Still another important factor in selecting a radioisotope for *in vivo* diagnosis is that the half-life of the radioisotope be long enough so that it is still detectable at the time of maximum uptake by the target, but short enough so that deleterious radiation with respect to the host is minimized. Ideally, a radioisotope used for *in vivo* imaging will lack a particle emission, but produce a large number of photons in the 140-250 keV range, which may be readily detected by conventional gamma cameras.

For *in vivo* diagnosis, radioisotopes may be bound to immunoglobulin, either directly or indirectly, by using an intermediate functional group. Intermediate functional groups which often are used to bind radioisotopes which exist as metallic ions to immunoglobulins are the bifunctional chelating agents such as diethylenetriaminepentacetic acid (DTPA) and ethylenediaminetetraacetic acid (EDTA) and similar molecules. Typical examples of metallic ions which can be bound to the monoclonal antibodies of the invention are ^{111}In, ^{97}Ru, ^{67}Ga, ^{68}Ga, ^{72}As, ^{89}Zr, and ^{201}Tl.

A monoclonal antibody useful in the method of the invention can also be labeled with a paramagnetic isotope for purposes of *in vivo* diagnosis, as in magnetic resonance imaging (MRI) or electron spin resonance (ESR). In general, any conventional method for visualizing diagnostic imaging can be utilized. Usually gamma and positron emitting radioisotopes are used for camera imaging and paramagnetic isotopes for MRI. Elements which are particularly useful in such techniques include ^{157}Gd, ^{55}Mn, ^{162}Dy, ^{52}Cr, and ^{56}Fe.

Kits for Detection of EPLIN

The materials for use in the method of the invention are ideally suited for the preparation of a kit. Such a kit may comprise a carrier means being compartmentalized to receive one or more container means such as vials, tubes, and the like, each of the container means comprising one of the separate elements to be used in the method. For example, one of the container means may comprise an EPLIN or *EPLIN* binding reagent, such as an antibody or nucleic acid, respectively. The constituents may be present in liquid or lyophilized form, as desired. Thus, the present invention also provides a kit useful for the detection of an EPLIN-specific cell component, the kit comprising carrier means containing one or more containers comprising a first container containing an EPLIN-specific binding reagent. As used herein, an "EPLIN-specific binding reagent" includes nucleic acids, such as probes, which hybridize to an EPLIN-specific cell component, such as DNA or RNA encoding the EPLIN protein. An EPLIN-specific binding reagent also includes proteins, such as antibodies, which bind to an EPLIN protein or fragment or derivative thereof. It is understood that an EPLIN-specific binding reagent includes any molecule which binds to an EPLIN-specific cell component such that the component can be identified.

One of the container means may comprise a probe which is or can be detectably labeled. Such probe may be an antibody or nucleotide specific for a target protein, or fragments thereof, or a target nucleic acid, or fragment thereof, respectively, wherein the target is indicative, or correlates with, the presence of EPLIN protein or EPLIN transcript. For example, oligonucleotide probes of the present invention can be included in a kit and used for examining the presence of EPLIN nucleic acid, as well as the quantitative (relative) degree of binding of the probe for determining the lack of binding (hybridizing) to the sequences, thus indicating the likelihood for an subject having a cell proliferation-associated pathology, such as, for example, cancer.

Where the kit utilizes nucleic acid hybridization to detect the target nucleic acid, the kit may also have containers containing nucleotide(s) for amplification of the target nucleic acid sequence. When it is desirable to amplify the target nucleic acid sequence, such as an EPLIN nucleic acid sequence, this can be accomplished using oligonucleotide(s) that are primers for amplification. For example, the kit may contain reagents necessary to perform RT-PCR on a sample containing, or suspected of containing, a cell harboring a pathogenic lentivirus such as HIV. Oligonucleotide primers based upon identification of the flanking regions contiguous with the target nucleotide sequence can be included in the kit such that the primers bind to an EPLIN transcript in the presence of, and under conditions that promote RT-PCR. The level of EPLIN transcript in a sample can be quantitated by means known to those of skill in the art.

The method of the invention provides the basis for a kit useful for the detection, or lack thereof, of a target EPLIN nucleic acid sequence in a sample obtained from a subject having, or suspected of having, a neoplasia. The absence, or under-production of, EPLIN transcript obtained from such a sample is indicative of the presence of a neoplasia. The kit includes a carrier means being compartmentalized to receive therein one or more containers. For example, a first container contains a nucleic acid primers which hybridize to the target nucleic acid (*e.g.*, EPLIN RNA) for the purpose of performing semi-quantitative RT-PCR. In addition, the kit can provide a nucleic acid probe for detection of an EPLIN RNA transcript. Thus, a first container contains a nucleic acid hybridization probe which hybridizes to the target nucleic acid.

Other target nucleic acid sequences of EPLIN can be determined by those of skill in the art. In addition, the kit may include a second container containing a means for detecting hybridization of the probe with the target nucleic acid. Such reporter means include a biotin-binding protein, such as avidin or streptavidin, bound to a reporter molecule, such as an enzymatic, fluorescent, or radionuclide label. Other reporter means and labels are well known in the art. The kit may also include an amplification polymerase and deoxyribonucleotide(s). The kit may further include nucleic acid amplification buffer. Preferably, the reagent that modifies unmethylated cytosine is bisulfite. The kit of the invention is intended to provide the reagents necessary to perform nucleic acid hybridization analysis as described herein.

Techniques for obtaining a sample containing, or believed to contain, neoplastic cells are usually based on collection of tissues containing such cells. Such tissue can include, for example, blood, lymph or other tissue. However, it is understood that the method of the invention is useful for detecting a neoplasia in any sample believed to contain such cells. Sample acquisition can be accomplished by any means which allows for the isolation of a sample from a subject that results in a sufficient quantity of fluid being obtained for testing.

The kit may also include a container containing antibodies which bind to a target protein, or fragments thereof. Thus, it is envisioned that antibodies which bind to EPLIN, or fragments thereof, can be included in a kit. In addition, the kit may include a second container containing a means for detecting binding of the antibody with the target EPLIN protein, or fragment thereof. Such reporter means include a biotin-binding protein, such as avidin or streptavidin, bound to a reporter molecule, such as an enzymatic, fluorescent, or radionuclide label. Other reporter means and labels are well known in the art.

Gene Therapy Methods

It has been observed that certain tumor cells return to normal function when fused with normal cells, suggesting that replacement of a missing factor, such as a wild-type tumor suppressor gene expression product may serve to restore a tumor cell to a normal state. These observations have led to research aimed at providing genetic treatment of tumor cells having defective tumor suppressor genes. Thus, in another aspect, the invention provides a

method for converting a neoplastic cell to a non-neoplastic state through the expression of wild-type levels of EPLIN.

Any of the methods known to the art for the insertion of DNA fragments into a vector, as described, for example, in Maniatis, T, Fritsch, E. F., and Sambrook, J. (1989): Molecular Cloning (a Laboratory manual), Cold Spring Harbor Laboratory, Cold Spring Harbor, New York; and Ausubel, F. M., Brent, R., Kingston, R. E., Moore, D. D., Seidman, J. G., Smith, J. a., and Struhl, K. (1992): Current Protocols in Molecular Biology, John Wiley & Sons, New York, may be used to construct EPLIN encoding gene expression vectors consisting of appropriate transcriptional/translational control signals and the desired EPLIN cDNA sequence downstream from the first in-frame AUG codon. These methods may include *in vitro* DNA recombinant and synthetic techniques and *in vivo* genetic recombination. Expression of a nucleic acid sequence encoding EPLIN may be regulated by a second nucleic acid sequence so that EPLIN is expressed in a host infected or transfected with the recombinant DNA molecule. For example, expression of EPLIN may be controlled by any promoter/enhancer element known in the art. The promoter activation may be tissue specific or inducible by a metabolic product or administered substance.

Promoters/enhancers which may be used to control EPLIN gene expression include, but are not limited to, the native EPLIN promoter, the cytomegalovirus (CMV) promoter/enhancer (Karasuyama, H. *et al.*, 1989, *J. Exp. Med.*, 169:13), the human beta-actin promoter (Gunning, P. *et al.*, 1987, *Proc. Natl. Acad. Sci. USA*, 84:4831), the glucocorticoid-inducible promoter present in the mouse mammary tumor virus long terminal repeat (HHTV LTR) (Klessig, D. F. *et al.*, 1984, *Mol. Cell Biol.*, 4:1354), the long terminal repeat sequences of Moloney murine leukemia virus (MULV LTR) (Weiss, R. *et al.*, 1985, RNA Tumor Viruses, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York), the SV40 early region promoter (Bernoist and Chambon, 1981, *Nature,* 290:304), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (RSV) (Yamamoto *et al.*, 1980, *Cell* 22:787), the herpes simplex virus (HSV) thymidine kinase promoter/enhancer (Wagner *et al.*, 1981, *Proc. Natl. Acad. Sci. U.S.A.*, 78:1441), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, *Nature*, 296:39), the adenovirus promoter (Yamada *et al.*, 1985, *Proc. Natl. Acad. Sci. U.S.A.*, 82:3567), and the herpes simplex virus LAT promoter (Wolfe, J. H. *et al.*, 1992, *Nature Genetics*, 1:379).

Expression vectors compatible with mammalian host cells for use in genetic therapy of tumor or cancer cells, include, but are not limited to: plasmids, retroviral vectors, adenovirus vectors, herpes viral vectors, and non-replicative avipox viruses, as disclosed, for example, by U.S. Pat. No. 5,174,993, incorporated herein by reference.

Methods of administering viral vectors are well known. In general, the skilled artisan will appreciate that a retroviral vector, an adenovirus vector, a plasmid vector, or any other appropriate vector capable of expressing the EPLIN protein can be administered *in vivo* to a neoplastic cell by a wide variety of manipulations. All such manipulations have in common the goal of placing the vector in sufficient contact with the target tumor to permit the vector to transduce or transfect the tumor cells. Neoplastic cells present in the epithelial linings of hollow organs may be treated by infusing the vector suspension into a hollow fluid filled organ, or by spraying or misting into a hollow air filled organ. Thus, the tumor cell may be present in or among the epithelial tissue in the lining of pulmonary bronchial tree, the lining of the gastrointestinal tract, the lining of the female reproductive tract, genitourinary tract, bladder, the gall bladder and any other organ tissue accessible to contact with the vector.

The EPLIN encoding gene construct of the present invention may be placed by methods well known to the art into an expression vector such as a plasmid or viral expression vector. A plasmid expression vector may be introduced into a tumor cell by calcium phosphate transfection, liposome (for example, LIPOFECTIN)-mediated transfection, DEAE Dextran-mediated transfection, polybrene-mediated transfection, electroporation and any other method of introducing DNA into a cell.

A viral expression vector may be introduced into a target cell in an expressible form by infection or transduction. Such a viral vector includes, but is not limited to: a retrovirus, an adenovirus, a herpes virus and an avipox virus. When EPLIN is expressed in any abnormally proliferating cell, the cell replication cycle is arrested, thereby resulting in senescence and cell death and ultimately, reduction in the mass of the abnormal tissue, *i.e.*, the tumor or cancer. A vector able to introduce the gene construct into a target cell and able to express EPLIN therein in cell proliferation-suppressing amounts can be administered by any effective method.

For example, a physiologically appropriate solution containing an effective concentration of active vectors can be administered topically, intraocularly, parenterally,

orally, intranasally, intravenously, intramuscularly, subcutaneously or by any other effective means. In particular, the vector may be directly injected into a target cancer or tumor tissue by a needle in amounts effective to treat the tumor cells of the target tissue.

Alternatively, a cancer or tumor present in a body cavity such as in the eye, gastrointestinal tract, genitourinary tract (*e.g.*, the urinary bladder), pulmonary and bronchial system and the like can receive a physiologically appropriate composition (*e.g.*, a solution such as a saline or phosphate buffer, a suspension, or an emulsion, which is sterile except for the vector) containing an effective concentration of active vectors via direct injection with a needle or via a catheter or other delivery tube placed into the cancer or tumor afflicted hollow organ. Any effective imaging device such as X-ray, sonogram, or fiberoptic visualization system may be used to locate the target tissue and guide the needle or catheter tube.

In another alternative, a physiologically appropriate solution containing an effective concentration of active vectors can be administered systemically into the blood circulation to treat a cancer or tumor that cannot be directly reached or anatomically isolated.

In yet another alternative, target tumor or cancer cells can be treated by introducing EPLIN protein into the cells by any known method. For example, liposomes are artificial membrane vesicles that are available to deliver drugs, proteins and plasmid vectors both *in vitro* or in vivo (Mannino, R. J. *et al.*, 1988, *Biotechniques*, 6:682) into target cells (Newton, A.C. and Huestis, W.H., *Biochemistry*, 1988, 27:4655; Tanswell, A.K. *et al.*, 1990, *Biochmica et Biophysica Acta*, 1044:269; and Ceccoll, J. *et al.*, *Journal of Investigative Dermatology*, 1989, 93:190). Thus, EPLIN protein can be encapsulated at high efficiency with liposome vesicles and delivered into mammalian cells *in vitro* or *in vivo*.

Liposome-encapsulated EPLIN protein may be administered topically, intraocularly, parenterally, intranasally, intratracheally, intrabronchially, intramuscularly, subcutaneously or by any other effective means at a dose efficacious to treat the abnormally proliferating cells of the target tissue. The liposomes may be administered in any physiologically appropriate composition containing an effective concentration of encapsulated EPLIN protein.

In one embodiment a tumor cell is transduced with a retrovirus vector, an adenovirus vector, a plasmid vector or any other appropriate vector capable of expressing the EPLIN protein in that tumor cell. The cancer cell may be present in a blood or bone marrow sample collected from a leukemia patient. A dose of EPLIN protein expressing retrovirus vector or

adenovirus vector or plasmid vector or any other appropriate vector is administered to the sample of blood or bone marrow at a dose sufficient to transduce enough cells in the sample to produce a reduction in tumor cell numbers. The cell proliferation of the treated cancer cells will be slowed or terminated followed by a process similar to normal cellular differentiation or cell senescence. Analogously, blood or bone marrow or other tissue is treated *ex vivo* using an effective dose of a liposome-encapsulated EPLIN protein. Thereafter the sample may be returned to the donor or infused into another recipient.

EXAMPLE 1
Materials and Methods

Cell Cultures

Human mammary epithelial cells (MEC) and normal human dermal fibroblasts were purchased from Clonetics. Breast cancer cell lines HBL-100, BT-20, SK-Br-3 and T-47D cells were cultured in RPMI 1640 medium supplemented with 10% fetal bovine serum (FBS) with T-47D cells receiving 1x ITS supplement (Sigma). MCF-7 and MDA-MB-231 cells were cultured in DMEM supplemented with 10% FBS. BeWo cells were cultured in Ham's F12K medium supplemented with 15% FBS.

Northern Blot Analysis and cDNA Cloning

10 μg total RNA isolated from cell cultures using RNA STAT-60 (Tel-Test) was used in Northern analysis as previously described (Chang *et al.*, *Oncogene*, 16:1921, 1998). Filter membranes were probed with cDNA clone #21 (corresponding to amino acids 268-462 of EPLIN-β) and hybridization signals were quantified on a phosphorimager (Molecular Dynamics). All probes were labeled with [^{32}P]-α-dCTP using a random prime labeling kit (Stratagene). Multiple tissue mRNA blots was purchased from Clontech and used in hybridization following the manufacturer's protocol. The cDNA insert from clone #21 was used as a probe to isolate full length EPLIN-α and -β cDNAs from a HeLa cell cDNA library. Two representative clones were fully sequenced to obtain approximately 3.6 kb of sequence.

Antibodies and Protein Analysis

The carboxy terminal region of EPLIN (aa 680-759 of EPLIN-β) was cloned into the pQE-30 vector (Qiagen) and expressed as a 6xHis-tagged fusion protein in *E. coli* strain XL-1 Blue. The recombinant protein was purified on Ni-NTA agarose under native conditions following the manufacturer's recommendations and used as immunogen for polyclonal rabbit anti-EPLIN antibodies (Covance Research Products).

Cell lysates used in immunoblot analyses were prepared by boiling tissue culture cells or minced tissues in 0.2 % SDS in TE (25 mM Tris-HCl, pH 7.5, 1 mM EDTA). 20 μg of cell lysates were separated by SDS-polyacrylamide gel electrophoresis and transferred to a nitrocellulose membrane. EPLIN isoforms were detected with polyclonal anti-EPLIN antibodies (1:10,000). To control the amounts of protein lysates, the filter membrane was also probed with a monoclonal anti-α-tubulin antibody (Sigma) at 1:2,000 dilution. Following incubation with a horseradish peroxidase-conjugated secondary antibody (Jackson ImmunoResearch), the immunoblots were developed using enhanced chemiluminescence (NEN).

Immunofluorescence

HOK18C and BeWo cells cultured on fibronectin-coated glass coverslips for 18 h were fixed in 3.7% formaldehyde (LADD Research) in PBS for 10 min and permeabilized in 0.2% Triton X-100 in PBS for 5 min. The slides were preincubated in a blocking buffer (0.1% Tween-20 + 10% goat serum in PBS) for 30 min before the addition of polyclonal anti-EPLIN antibodies (1:200 dilution). All incubations were performed at room temperature. HOK18C cells were labeled with Texas Red-conjugated goat anti-rabbit IgG secondary antibody (Jackson ImmunoResearch) and Oregon Green phalloidin (Molecular Probes) while BeWo cells were labeled with fluorescein isothiocyanate-conjugated goat anti-rabbit IgG secondary antibody (Jackson ImmunoResearch) and Texas Red phalloidin (Molecular Probes). Coverslips were mounted with ProLong Antifade (Molecular Probes) and viewed under a fluorescence microscope (Nikon). Pre-immune sera did not produce a staining pattern.

Conditional Expression of EPLIN

U2-OS cells were transfected with the plasmid pTet-On (Clontech) to create U2-OS Tet-On cells expressing tetracycline-inducible transactivator. EPLIN-α and -β cDNAs were cloned into the pTRE vector (Clontech) that has been modified by the insertion of an amino terminal FLAG epitope and multiple cloning sites. pTRE-FLAG-EPLIN-α or -β and pBABEpuro (Morgenstern and Land, *Nucleic Acids Res.*, 18:587, 1990) plasmids were co-transfected into the U2-OS cells and the stable transfectants were selected with puromycin (1 mg/ml). The expression of EPLIN in stable cell lines was induced by the addition of 0.5 mg/ml doxycycline (Sigma). Morphological changes were observed 48 h after the induction of EPLIN. Cell growth was determined by a tetrazolium dye colorimetric assay (Denizot and Lang, *J. Immunological Methods*, 89:271, 1986) with the following modifications. Cells were incubated for 3.5 h in phenol red-free RPMI 1640 medium (Sigma) with 1 mg/ml MTT (3-[4,5-dimethylthiazol-2-y]-2,5-diphenyl tetrazolium bromid) (Sigma) and the formazan product was solubilized in isopropanol containing 0.04 N hydrochloric acid and 1% Triton X-100.

Figure 1A is a schematic diagram of two EPLIN cDNAs. The sequence of two isoforms diverges at the 5' end (indicated by the stripped and dotted boxes). The EPLIN-β unique sequences allow the extension of the ORF by 160 aa at the amino terminus of EPLIN-α. The positions of in frame stop codons upstream to the AUG start codons for two EPLIN isoforms and the termination codons are denoted. Figure 1B shows the deduced amino acid sequence of EPLIN-β. The ORF of EPLIN-α starts at aa position 161 of EPLIN-β. The aa sequences of two EPLIN isoforms are identical except for Arg344 of EPLIN-β which has been replaced by Pro184Gly185 in EPLIN-α. The 52 aa sequence of a LIM domain is underlined. Figure 1C shows the alignment of the EPLIN LIM domain sequence with the LIM domain of the mutant SREBP-2, KIAA0750, plant transcription factor SF3, and muscle LIM protein. The signature cysteine and histidine residues of LIM domain are indicated by bold lettering. Amino acid sequence identities (o) and similarities (underlined) are indicated.

Figure 2A shows the distribution of EPLIN expression in different human adult tissues as determined by a Northern analysis. Filters containing mRNA from multiple human tissues (Clontech) were used for Northern blotting. The positions of ~8 kb and ~3.8 kb

transcripts hybridized by the EPLIN probe are indicated (top). The same blot was re-probed with human b-actin cDNA (bottom).

Figure 2B shows the expression of EPLIN in different human primary cells were examined by an immunoblot analysis. MEC: mammary epithelial cells. PrEC: prostate epithelial cells. NHOK: normal human oral keratinocytes. Ao. Endo.: aortic endothelial cells. Fibroblasts: Dermal fibroblasts. Myocardium: human left ventricle. The positions of EPLIN-α and -β are noted. The loading of equivalent amounts of cell lysates was confirmed by probing the filter membrane with anti-a tubulin antibody.

Figure 3A shows the expression of EPLIN transcripts in HPV-immortalized oral keratinocyte cell lines (HOK18A-C and HOK16B), tumorigenic HPV-transformed oral keratinocyte cell line (HOK16B-BapT), and oropharyngeal cancer cells (Tu-177, HEp2, and SCC-9) was determined by a Northern analysis (top). The filter membrane was re-probed with human G3PDH cDNA (bottom). The expression of EPLIN, normalized against the G3PDH, in each cell line is indicated. Figure 3B shows the expression of EPLIN proteins in different prostate cancer cell lines and xenograft tumors was determined by an immunoblot analysis. PrEC: prostate epithelial cells. PC3 and DU145: PSA-negative prostate cancer cell lines. LnCAP, LAPC3, LAPC4, and LAPC9: PSA-positive prostate cancer cells or xenograft tumors. The positions of EPLIN-α and -β are noted. The loading of equivalent amounts of cell lysates was confirmed by probing the filter membrane with anti-a tubulin antibody. Figure 3C shows the expression of EPLIN proteins in different breast cancer cell lines was determined by an immunoblot analysis. MEC: mammary epithelial cells. IMEC: immortalized mammary epithelial cells. HBL-100 is a non-tumorigenic breast cancer cells, while BT-20, SK-Br-3, MCF-7, T-47D, and MDA-MB-231 are tumorigenic breast cancer cell lines. The positions of EPLIN-α and -β are noted. The loading of equivalent amounts of cell lysates was confirmed by probing the filter membrane with anti-a tubulin antibody. Figure 3D shows the expression of EPLIN transcripts in different breast cancer cell lines was determined by a Northern analysis (top). The filter membrane was re-probed with human G3PDH cDNA (bottom). The expression of EPLIN, normalized against the G3PDH, in each cell line is indicated.

Figure 4A shows the relative amount of EPLIN isoforms in HOK18C (an HPV-immortalized human oral keratinocyte cell line) and BeWo (a human choriocarcinoma cell

line) was determined by an immunoblot analysis. EPLIN-α is expressed as the major isoform in HOK18C, while EPLIN-β is the major isoform in BeWo. Figures B-E show the subcellular localization of EPLIN was determined by *in situ* immunofluorescence using anti-EPLIN antibodies (B and D). The staining pattern of anti-EPLIN antibodies (B and D) overlapped with the staining of actin stress fibers (C and E). Texas Red-conjugated goat anti-rabbit IgG secondary antibody (B) and fluorescein isothiocyanate-conjugated goat anti-rabbit IgG secondary antibody (D) were used to detect EPLIN. The stress fibers were stained with Oregon Green-phalloidin© and Texas Red-phalloidin (E).

Figures A-D show the U2-OS osteosarcoma cells were engineered to express either EPLIN-α or -β isoform under the control of a tetracycline-inducible promoter (Tet-On). The appearance of U2-OS cells cultured with (B and D) and without (A and C) the induction of EPLIN are shown. Note that the expression of EPLIN changed the morphology of the U2-OS cells from round polygonal cells to fusiform cells characterized by asymmetric cytoplasmic extensions. Figure 5E shows the levels of EPLIN expression in the U2-OS cells cultures minus (no induction) and plus (induction) doxycycline were determined by an immunoblot analysis using anti-EPLIN antisera. Lane 1, parental U2-OS (Tet-on) cells; lane 2, U2-OS (EPLIN-α) cells before the induction; lane 3 and 4, U2-OS (EPLIN-α) and U2-OS (EPLIN-β) cells 48 h after the induction. Figure 5F shows the growth of U2-OS cells is presented as the ratio of cell numbers with and without EPLIN induction. For each time point, cell growth in triplicates were determined by a tetrazolium dye inclusion method.

EXAMPLE 2

cDNA fragments containing a partial open reading frame (ORF) were identified by the presence of a LIM domain. Clone #21 was used as a probe to isolate several cDNA clones from a HeLa cell cDNA library. Sequence analysis of these cDNA clones allowed us to assemble an ORF of 600 aa (EPLIN-α) and an isoform (EPLIN-β) that extended an additional 160 aa at the amino terminus (Fig 1A and 1B). The EPLIN-β mRNA also contained a deletion of 3 nucleotides within the coding region, introducing an Arg in place of ProGly at the corresponding position of EPLIN-α. Southern analysis indicated that EPLIN is a single copy gene, suggesting that the two EPLIN isoforms are generated by an alternative pre-RNA processing event. The predicted amino acid sequence of EPLIN was notable for a

single centrally located LIM domain that is homologous to the partial ORF of a hamster gene of an unknown function. The EPLIN LIM domain is distantly related to the LIM domains of plant transcription factors SF-3 and the muscle LIM protein (Fig 1C). Outside the LIM domain, EPLIN is unique in sequence, displaying no significant homology to known proteins or recognizable motifs.

Northern blot analysis of poly (a)+-RNA derived from normal human adult tissues demonstrated the expression of two EPLIN transcripts of ~3.8 kb and ~8 kb in size (Fig 2A). The highest level of EPLIN mRNA was observed in placenta, followed by kidney, pancreas, prostate, ovary, spleen, and heart. A low level of EPLIN mRNA was also detected in all other tissues. The ORFs for both EPLIN-α and -β can be assembled from cDNA clones with insert sizes of ~3.6 kb, corresponding the ~3.8 kb transcript seen on the Northern blot.

Polyclonal anti-EPLIN antisera directed against the carboxy-terminal region common to both α and β isoforms was prepared. In normal primary mammary (MEC), prostate (PrEC), and oral (NHOK) epithelial cells, anti-EPLIN antisera detected a major protein band of 90 kD and a second minor species of 110 kD in molecular weight (Fig 2B). These two species were assigned EPLIN-α and EPLIN-β, respectively.

A Northern analysis of immortalized or transformed oropharyngeal cell lines confirmed a consistent down-regulation of EPLIN transcripts to 10 to 60 % of the level seen in the NHOK (Fig 3A). An immunoblot analysis demonstrated a reduction in EPLIN protein in these cell lines. Using anti-EPLIN antisera, we extended the expression analysis of EPLIN to different types of human cancers. An immunoblot analysis using cell lysates prepared from 4 human prostate cancer cell lines showed significant changes of EPLIN expression (Fig 3B). In two PSA-negative prostate cancer cell lines, PC3 and DU145, EPLIN expression was detectable, but at significantly reduced levels compared to the level seen in the normal primary prostate epithelial cells (PrEC). In two PSA-positive prostate cancer cell lines, LnCap and LAPC4, the expression of EPLIN-α was not detectable, while EPLIN-β continued to be expressed at a level comparable to that in the PrEC. Examination of human prostate tumors propagated in SCID mice also demonstrated the loss of EPLIN-α expression in LAPC3, LAPC4, and LAPC9 xenografts.

A survey of breast cancer cell lines revealed a similar change in EPLIN expression (Fig 3C). Both immortalized mammary epithelial cells (IMEC) and HBL-100, a non-

tumorigenic breast cancer cell line, expressed EPLIN-α and -β isoforms at levels equivalent to that seen in the MEC. In the BT-20 breast cancer cells, there was a reduction in EPLIN-α accompanied by an increase in EPLIN-β. A similar increase EPLIN-β expression was also seen in the SK-Br-3 breast cancer cells which lacked the EPLIN-α expression. In three other breast cancer cell lines, EPLIN-α was either absent (MCF-7 and T-47D) or significantly reduced (MDA-MB-231), while EPLIN-β continued to be expressed at a level equivalent to that in the MEC. A Northern analysis demonstrated a reduction in EPLIN transcripts in all of the breast cancer cell lines, confirming that the loss of EPLIN proteins is due to a transcriptional down-regulation (Fig 3D).

EPLIN is a cytoskeletal protein that can alter cell morphology and suppress cell proliferation.

To investigate the potential function of EPLIN, the subcellular distribution of endogenous EPLIN was determined. Since the available polyclonal anti-EPLIN antisera do not distinguish the two known isoforms of EPLIN, *in situ* immunofluorescence was performed using two different cell lines, HOK18C (an immortalized human oral keratinocyte line), and BeWo (a human choriocarcinoma cell line). EPLIN-α is expressed as the predominant form in HOK18C, while EPLIN-β is the predominant form in BeWo (Fig 4A). *In situ* immunofluorescence analysis demonstrated the localization of both EPLIN-α and -β to the cytoplasm in a fibrillar pattern at the periphery of the cell (Fig 4B and D). This pattern of staining is similar to the staining of actin fibers with phalloidin (Fig 4C and E). In addition, there was an overlap in the EPLIN staining to the paxillin staining (data not shown), suggesting that EPLIN is a component of the focal adhesion plaque.

To identify the effect of EPLIN on cell growth, each isoform was expressed in U2-OS osteosarcoma cells under the control of a tetracycline-inducible promoter. U2-OS cells, like most other cells, express EPLIN-α as the major isoform and a small amount of EPLIN-β isoform (Fig 5E). Ectopic expression of either EPLIN isoform altered the morphology of the U2-OS cells from round polygonal cells with a cobblestone appearance to larger fusiform cells with spindle cell features and cytoplasmic extensions (Fig 5A-D). In addition, the EPLIN overexpressing cells required a longer incubation time in trypsin for detachment, suggesting a change in the cell-matrix interaction. An analysis of cell proliferation using a

tetrazolium dye inclusion assay revealed that the induction of EPLIN-β suppresses cell growth (Fig 5F). While the effect was not as pronounced, a growth inhibition was also seen when EPLIN-α was overexpressed.

The present invention provides a novel gene, EPLIN, that is down-regulated in human cancer cells. Although the expression of EPLIN varied considerably in different adult tissues, there was a general tendency of higher expression in tissues rich in epithelial cells. This preferential expression of EPLIN in epithelial cells was substantiated by an immunoblot analysis demonstrating high levels of EPLIN expression in the normal epithelial cells (*e.g.*, MEC, PrEC, NHOK). Low levels of EPLIN were also detected in the primary aortic endothelial cells and fibroblasts, but not in the myocardium. The absence of EPLIN proteins in the myocardium, in view of the relative abundance of EPLIN transcripts in the same tissue, suggest that the steady state level of EPLIN proteins can be subjected to a posttranslational regulation. The reduction in EPLIN protein in cancer cells in general paralleled the reduction in EPLIN transcripts (see Fig 3C and D).

EPLIN sequence analysis revealed a single centrally located LIM domain. This motif may allow EPLIN to interact with other cellular proteins. Several LIM domain proteins have been implicated in cellular transformation. LMO-2 (formerly called RBTN2/TTG2), which interacts with the basic-helix-loop-helix protein Tal/Scl, is aberrantly expressed in acute T-cell leukemia as a result of chromosomal rearrangement and can promote T-cell tumors (Rabbitts, *Genes and Devel.*, 12:2651, 1998). ril and DRAL are proteins of unknown function that are transcriptionally down-regulated in Ras-transformed cells and rhabdomyosarcoma cells, respectively (Kiess *et al.*, *Oncogene*, 10:61, 1995; Genini *et al.*, *DNA and Cell Biol.*, 16:433, 1997). Many LIM domain proteins are involved in cell lineage determination as DNA-binding transcription factors or accessory factors that associate with DNA-binding transcription factors to modulate gene transcription (Dawid *et al.*, *Trends in Genetics*, 14:156, 1998). Other LIM domain proteins interact with cytoskeletal proteins or localize to the site of cell-matrix attachment. This class of LIM domain proteins includes zyxin (Beckerle, *Bioessays*, 19:949, 1997); paxillin, hic-5, and leupaxin (Brown *et al.*, *J. Cell Biol.*, 135:1109, 1996); LIM-kinase (Yang *et al.*, *J. Biol. Chem.*, 270:12152, 1998); and limatin (Roof *et al.*, *J. Cell Biol.*, 138:575, 1997). The amino acid sequence of the EPLIN

LIM domain is closely related to the LIM domain of the plant transcription factor SF3 (48% aa identity; 73% aa similarity within the 52 aa LIM domain).

In situ immunofluorescence studies showed localization of both EPLIN-α and -β isoforms to filamentous actin-rich areas at the periphery of the cell. Furthermore, there was a frequent overlap between EPLIN staining and paxillin staining, suggesting that EPLIN maybe present in the focal adhesion plaques as well. The overexpression of EPLIN appears to affect the cell-matrix interactions as evidenced by changes in cell morphology. While the subcellular localization of endogenous EPLIN-α and -β isoforms was indistinguishable, ectopic expression of EPLIN-β had a more pronounced effect on the growth of U2-OS cells, suggesting a potential functional difference between the two EPLIN isoforms.

EPLIN expression is down-regulated in the majority of cancer cell lines examined in the present study, indicating that the loss of EPLIN expression is directly linked to cellular transformation. Breast and prostate cancer cells, but not the oropharyngeal cancer cells, exhibited a specific loss of EPLIN-α isoform. The loss of EPLIN-α isoform was accompanied by an increase in EPLIN-β isoform in 2/6 breast cancer cell lines (*e.g.*, BT-20 and SK-Br-3). The combined levels of the two EPLIN isoforms were lower in BT-20 and SK-Br-3 cells.

The major difference between the two EPLIN isoforms is at the amino terminus where the b isoform contains an extension of 160 aa. The sequence divergence may be an alternative pre-mRNA splicing event involving a single pre-mRNA that utilizes alternative exons. Alternatively, EPLIN is transcribed from two distinct promoters to generate two pre-mRNA species both of which are spliced to the common 3' exons. The relative increase in EPLIN-β in breast cancer cell lines BT-20 and Sk-Br-3, which have lost the expression of EPLIN-α, indicates that the expression of the two EPLIN isoforms can be regulated independently.

EPLIN-α Nucleic Acid Sequence (SEQ ID NO:1)

gctttctccatgtggcaaggctgtaactgttcacagctgtctgaaacagcagtggaccaggagcagcttggagttttaactttcattttaca
aagaacaacatgtttgaatgtttcagcaggcaagttataactggcatctacttcttgttcttctagaacaccgaaaatctctcccagcacttt
agaaaggggaccctgactgtgttaaagaagaagtgggagaacccagggctgggagcagagtctcacacagactctctacggaaca
gcagcactgagattaggcacagagcagaccatcctcctgctgaagtgacaagccacgctgcttctggagccaaagctgaccaagaa
gaacaaatccaccccagatctagactcaggtcacctcctgaagccctcgttcagggtcgatatccccacatcaaggacggtgaggatc
ttaaagaccactcaacagaaagtaaaaaaATGGAAAATTGTCTAGGAGAATCCAGGCATGAAGTAG
AAAAATCAGAAATCAGTGAAAACACAGATGCTTCGGGCAAAATAGAGAAATATAA
TGTTCCGCTGAACAGGCTTAAGATGATGTTTGAGAAAGGTGAACCAACTCAAACT
AAGATTCTCCGGGCCCAAAGCCGAAGTGCAAGTGGAAGGAAGATCTCTGAAAAC
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EPLIN-β Amino Acid Sequence (SEQ ID NO:4)

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TQNQKSQDVELWEGEVVKELSVEEQIKRNRYYDEDEDEE

It will be apparent to those skilled in the art that various modifications and variations can be made to the compositions and processes of this invention. Thus, it is intended that the present invention cover such modifications and variations, provided they come within the scope of the appended claims and their equivalents.

WHAT IS CLAIMED IS:

1. A substantially purified EPLIN polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or SEQ ID NO:4.

2. A substantially purified polypeptide comprising an amino acid sequence encoded by a nucleic acid sequence which hybridizes to the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:3 under stringent conditions.

3. An isolated polynucleotide encoding an amino acid sequence as set forth in SEQ ID NO:2 or SEQ ID NO:4.

4. An isolated polynucleotide selected from the group consisting of:
   (a) SEQ ID NO:1 or SEQ ID NO:3;
   (b) SEQ ID NO:1 or SEQ ID NO:3, wherein T can also be U;
   (c) nucleic sequences complementary to SEQ ID NO:1 or SEQ ID NO:3; and
   (d) fragments of (a), (b), or (c) that are at least 15 bases in length and that will hybridize to DNA which encodes a polypeptide of SEQ ID NO:2 or SEQ ID NO:4.

5. An expression vector containing the polynucleotide of claim 3.

6. The expression vector of claim 5, wherein the vector is a plasmid.

7. The expression vector of claim 5, wherein the vector is a viral vector.

8. The polynucleotide of claim 3, wherein the polynucleotide sequence is from

9. A host cell transformed with an expression vector of claim 5.

10. The host cell of claim 9, wherein the cell is a eukaryotic cell.

11. The host cell of claim 9, wherein the cell is a prokaryotic cell.

12. A method of producing EPLIN polypeptide comprising:

(a) transforming a host cell with a polynucleotide of claim 2;

(b) expressing the polynucleotide in the host; and

(c) recovering the EPLIN polypeptide.

13. The method of claim 12, wherein the host cell is a prokaryotic cell.

14. An antibody that binds to the polypeptide of claim 1.

15. The antibody of claim 14, wherein the antibody is polyclonal.

16. The antibody of claim 15, wherein the antibody is monoclonal.

17. A method for identifying a compound which binds to EPLIN polypeptide comprising:

(a) incubating components comprising the compound and EPLIN polypeptide under conditions sufficient to allow the components to interact; and

(b) measuring the binding of the compound to EPLIN polypeptide .

18. The method of claim 17, wherein the compound is a peptide.

19. The method of claim 17, wherein the compound is a peptidomimetic.

20. The method of claim 17, wherein the compound is an antibody.

21. A method of detecting a neoplastic cell in a sample comprising:

contacting a sample suspected of containing a neoplastic cell with a reagent that binds to an EPLIN-specific cell component; and

detecting binding of the reagent to the component.

22. The method of claim 21, wherein the neoplastic cell is an epithelial cell.

23. The method of claim 21, wherein the EPLIN-specific component is nucleic acid which encodes EPLIN polypeptide, or fragments thereof.

24. The method of claim 23, wherein the nucleic acid is DNA.

25. The method of claim 23, wherein the nucleic acid is RNA.

26. The method of claim 25, wherein the EPLIN-specific cell component is the EPLIN polypeptide, or fragments thereof.

27. The method of claim 25, wherein the reagent is a probe.

28. The method of claim 27, wherein the probe is nucleic acid.

29. The method of claim 27, wherein the probe is an antibody.

30. The method of claim 29, wherein the antibody is polyclonal.

31. The method of claim 29, wherein the antibody is monoclonal.

32. The method of claim 27, wherein the probe is detectably labeled.

33. The method of claim 32, wherein the label is selected from the group consisting of a radioisotope, a bioluminescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate, or an enzyme.

34. The method of claim 21, wherein the sample is obtained from a subject selected from the group consisting of human, swine, porcine, feline, canine, equine, murine, cervine, caprine, lupine, leporidine and bovine.

35. A method of detecting a cell proliferative disorder in a sample from a subject, comprising:

contacting a first sample having, or suspected of having, a cell proliferative disorder with a reagent that binds to an EPLIN-specific cell component and detecting binding of the reagent to the component;

contacting a second cell not having a cell proliferative disorder with a reagent that binds to an EPLIN-specific cell component and detecting binding of the reagent to the component;

comparing the level of binding of the reagent in the first sample with the level of binding of the reagent in the second sample, wherein a decreased level of binding of the reagent to an EPLIN-specific cell component from the first sample is indicative of a cell proliferative disorder.

36. The method of claim 35, wherein the EPLIN-specific cell component is nucleic acid which encodes the EPLIN polypeptide.

37. The method of claim 35, wherein the EPLIN-specific cell component is the EPLIN protein, or fragments thereof.

38. The method of claim 36, wherein the nucleic acid is RNA.

39. The method of claim 35, wherein the reagent is a probe.

40. The method of claim 39, wherein the probe is nucleic acid.

41. The method of claim 39, wherein the probe is an antibody.

42. The method of claim 41, wherein the antibody is a human antibody.

43. The method of claim 41, wherein the antibody is polyclonal.

44. The method of claim 41, wherein the antibody is monoclonal.

45. A kit useful for the detection of an EPLIN-specific cell component, the kit comprising carrier means containing one or more containers comprising a first container containing an EPLIN-specific binding reagent.

46. A method for ameliorating a cell proliferative disorder associated with EPLIN activity, comprising treating a subject having the disorder with a compound that regulates EPLIN activity.

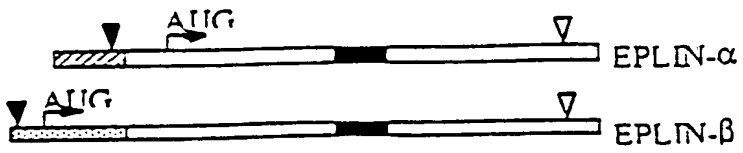
47. The method of claim 46, wherein the cell proliferative disorder is selected from the group consisting of cancer, atherosclerosis, Gaucher disease, scleroderma, arthritis and liver cirrhosis.

48. The method of claim 46, wherein the compound that regulates EPLIN activity is a protagonist of EPLIN.

49. A method for ameliorating a cell proliferative disorder associated with EPLIN, comprising treating a subject having the disorder, at the site of the disorder, with a composition which regulates EPLIN activity.

FIGURE 1

(A)



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(C)

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KIAA0750  .YF.K.R..V....S.EGHF..RE.....I.ATT.R.AA.TFDCDE.KF.....
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FIGURE 2

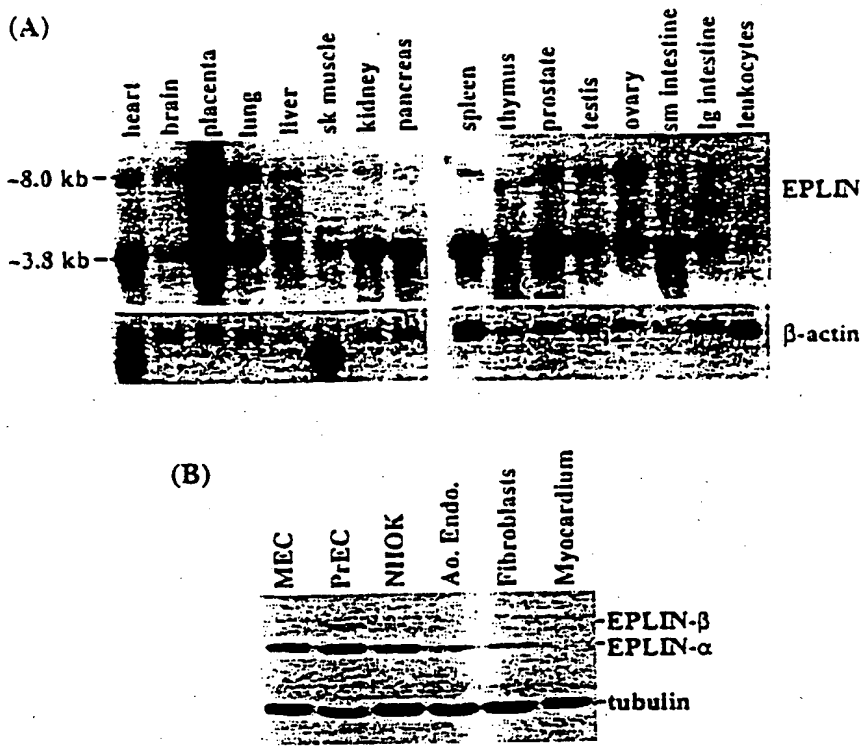


FIGURE 3

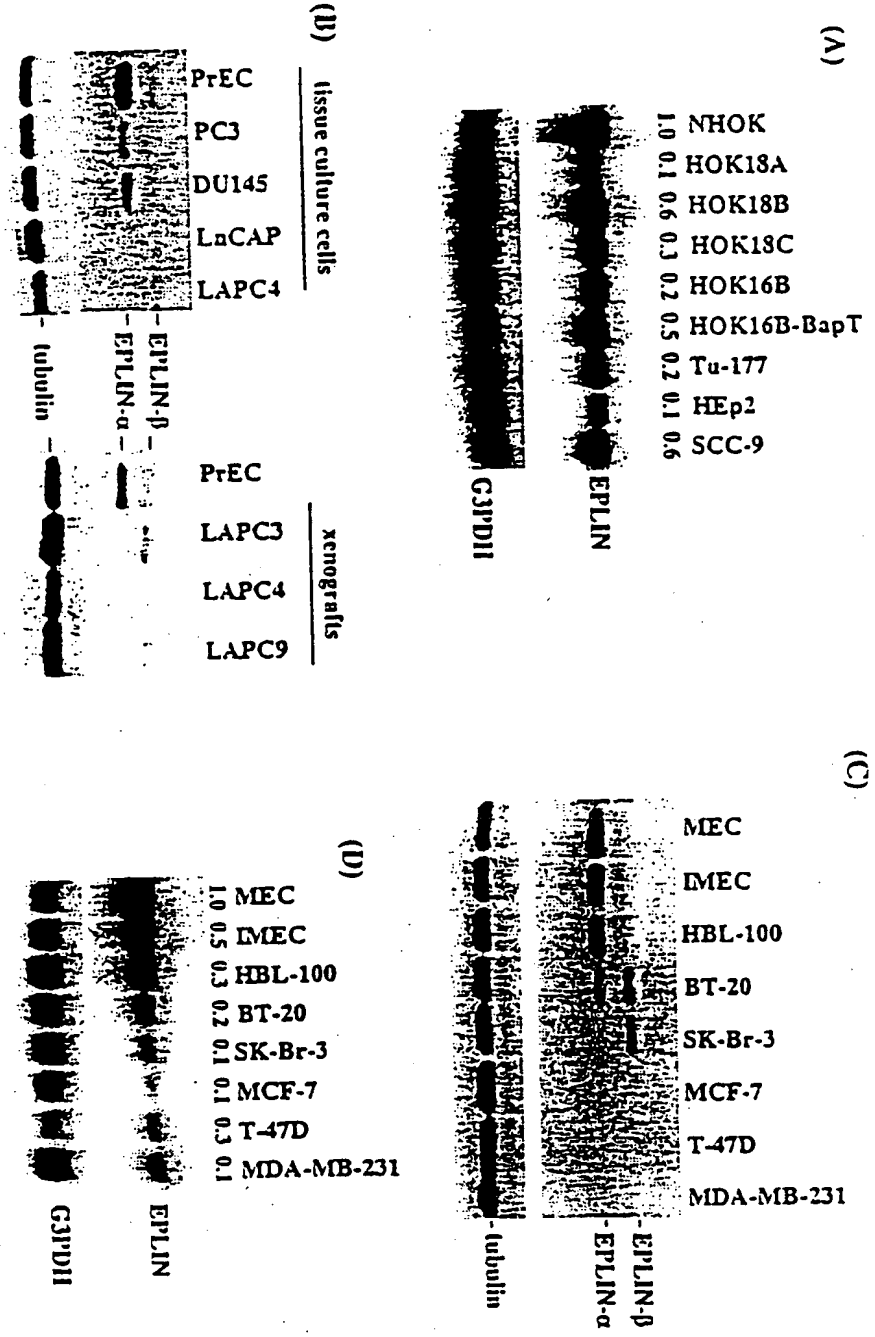
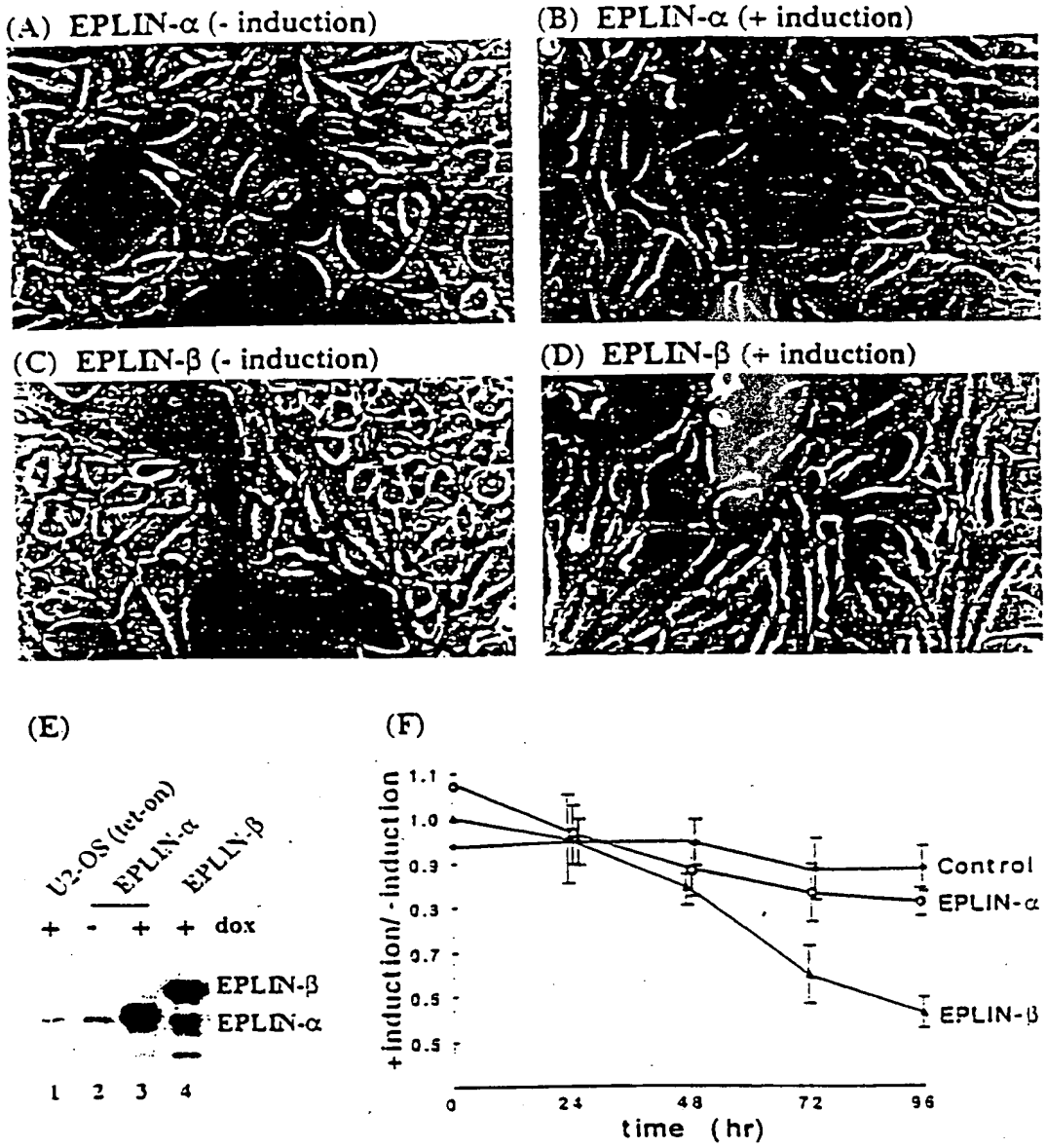


FIGURE 4

FIGURE 5



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/24689

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/02; C12Q 1/68; C07K 17/00
US CL : 536/23.1; 435/6; 530/350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 536/23.1, 23.5; 424/277.1; 435/6, 7.1; 514/2; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	MAUL et al. EPLIN, Epithelial protein lost in neoplasm. Oncogene. October 1999, Vol. 18, pages 7838-7841, entire document and sequence.	1-49
X,P	CHEN et al. Characterization of the human EPLIN (Epithelial Protein Lost in Neoplasm) gene reveals distinct promoters for the two EPLIN isoforms. Gene. 02 May 2000, Vol. 248, pages 69-76, entire document and sequence.	1-49
A	US 4,708,948 A (IWATA et al) 24 November 1987.	1-49

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
	28 DEC 2000
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Richard Schwartz Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/24689

Continuation of B. FIELDS SEARCHED Item3: STN (Medline, Caplus, Registry, Biosis,PATDPA, PATOSDE), EAST, Sequence Search (Issued_Patents, N_Geneseq_36, GenEbl, A_Geneseq_36, SPTREMBL_14)